

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2006, 14:25:10 ; Search time 1573 Seconds  
(without alignments)

10824.596 Million cell updates/sec

Title: US-10-612-594-1

Perfect score: 9100

Sequence: 1 accggtgcgaggaggaaca.....cagtccttcaagggtgga 9100

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	138.4	1.5	5511	3	US-08-928-361B-2
C 2	138.4	1.5	5511	3	US-09-588-995A-2
C 3	138.4	1.5	7334	3	US-08-928-361B-1
C 4	138.4	1.5	7334	3	US-09-588-995A-1
C 5	125	1.4	5163	3	US-08-700-651-1
C 6	125	1.4	5163	3	US-08-928-361B-4
C 7	125	1.4	5163	3	US-09-588-995A-4
C 8	125	1.4	5318	3	US-08-700-651-2
C 9	125	1.4	5318	3	US-08-928-361B-3
C 10	125	1.4	5318	3	US-09-588-995A-3
C 11	113.8	1.3	3486	3	US-09-614-221A-292
C 12	110.8	1.2	867	3	US-09-216-393B-340
C 13	110.8	1.2	867	3	US-09-216-393B-342
C 14	110.8	1.2	1397	3	US-09-216-393B-343
C 15	110.8	1.2	1397	3	US-09-216-393B-345
C 16	103.2	1.1	601	3	US-09-949-016-180704
C 17	103.2	1.1	70770	3	US-09-949-016-16938
C 18	98	1.1	83428	3	US-09-949-016-13610
C 19	95.6	1.1	8045	5	US-09-913-878A-1
C 20	90.6	1.0	19124	2	US-08-487-826B-13
C 21	82.8	0.9	8442	3	US-09-272-032-6
C 22	80.2	0.9	7218	2	US-08-232-463-14
C 23	79.8	0.9	1037	3	US-09-181-585-3

C 24	79.8	0.9	1159	3	US-09-181-585-1	Sequence 1, Appli
C 25	79.8	0.9	1471	3	US-09-181-585-2	Sequence 2, Appli
C 26	79.4	0.9	43795	3	US-08-742-185-101	Sequence 101, App
C 27	78.6	0.9	1671	3	US-09-248-796A-8235	Sequence 8235, Ap
C 28	78	0.9	2032	3	US-09-241-581B-5	Sequence 5, Appli
C 29	78	0.9	2032	3	US-08-265-428-5	Sequence 5, Appli
C 30	78	0.9	2032	7	PCT-US95-07721-5	Sequence 5, Appli
C 31	77	0.8	1149	3	US-09-248-796A-9133	Sequence 9133, Ap
C 32	76.6	0.8	147382	3	US-09-949-016-14624	Sequence 14624, A
C 33	76.4	0.8	3001	3	US-09-539-333D-215	Sequence 215, App
C 34	75.2	0.8	3337	2	US-08-072-610-1	Sequence 1, Appli
C 35	75.2	0.8	3337	2	US-08-713-822B-1	Sequence 1, Appli
C 36	75.2	0.8	3337	3	US-09-092-458-1	Sequence 1, Appli
C 37	75.2	0.8	3337	3	US-08-719-821C-1	Sequence 1, Appli
C 38	74.8	0.8	740	3	US-09-451-117-1	Sequence 1, Appli
C 39	74.8	0.8	740	3	US-09-888-655-1	Sequence 1, Appli
C 40	74.8	0.8	740	3	US-09-888-501-1	Sequence 1, Appli
C 41	74.6	0.8	1485	3	US-09-248-796A-2443	Sequence 2443, Ap
C 42	74.2	0.8	1671	3	US-09-614-221A-554	Sequence 554, App
C 43	74.2	0.8	1671	3	US-09-487-558B-425	Sequence 425, App
C 44	74	0.8	52202	3	US-09-949-016-17006	Sequence 17006, A
C 45	73.8	0.8	198	7	PCT-US95-10668-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-08-928-361B-2/C  
; Sequence 2, Application US/08928361B  
; Patent No. 6071518  
; GENERAL INFORMATION:  
; APPLICANT: Petersen, Carolyn  
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,  
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS  
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM  
; TITLE OF INVENTION: SPECIES INFECTIONS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PETERS, VERNY, JONES & BIKSA  
; STREET: 385 Sherman Avenue, Suite 6  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306-1840  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/928,361B  
; FILING DATE: 12-SEP-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026,062  
; FILING DATE: 13-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: VERNY, Hana  
; REGISTRATION NUMBER: 30,518  
; REFERENCE/DOCKET NUMBER: 480.76-1(HV)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-1677  
; TELEFAX: 650-324-1678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5511 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-928-361B-2